Remarks

The specification has been amended only to direct the entry of this corrected Sequence Listing at the end of the above identified application and to provide the SEQ ID NO's next to the specific sequence. The change made in the sequence listing does not include new matter.

In accordance with 37 C.F.R. § 1.821(g), this submission includes no new matter.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith in the above application are the same.

Applicants respectfully request that the substitute Sequence Listing submitted herewith be introduced into the captioned application.

It is respectfully believed that the present application is in condition for examination. Early notice to this effect is earnestly solicited. If the Examiner believes, for any reason, that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

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Version With Markings to Show Changes Made

In the Specification:

At page 15, the paragraph starting at line 22 and ending on page 16, line 2, was replaced with the following:

> We constructed a second vector pGSTN by first PCR-amplifying the *Schistosoma japonicum* glutathione *S* transferase (GST) gene from pGEX-2T (Pharmacia) under standard conditions using primers 'GSTfwd2' (5'-ATG CTG CAG ACG TCA ACA GTA TCC ATG GCC CCT ATA CTA GG-3') (SEQ ID NO: 1) and 'GSTHindIII' (5'-GCG AGG AAG CTT GTC AAT CAG TCA CGA TGA ATT CCC G-3') (SEQ ID NO: 2). These primers introduce an *Nco* I restriction site at the start codon of GST, mutate the second residue of GST from serine to alanine, and introduce a stop codon in the multiple cloning site 3'- of the GST gene followed by a *Hin* dIII restriction site. The PCR product was then cloned under standard conditions as an *Nco* I/*Hin* dIII fragment into pTrcHisA (Invitrogen) previously digested with *Nco* I/*Hin* dIII to generate pGSTN.

At page 16, the paragraph starting at line 7 and ending at line 17 was replaced with the following:

> We amplified the GST gene from the construct pGSTN using the polymerase chain reaction with custom-designed vector-specific primers 'STforward' (5'-ATG CTG ACG TCA TGA GGC CCA TGG GGC CCG GAT AAC AAT TTC ACA CAG G-3') (SEQ ID NO: 3) and 'STreverse' (5'-GCG GAT CCT TGC GGC CGC CAG GCA AAT TCT GTT T-3') (SEQ ID NO: 4) which bind to the vector 156 bp upstream of the start and 84 bp downstream of the stop codons respectively. 30 cycles of PCR (94°C 1min; 57°C 1min; 72°C 2min) were carried out in four separate 100μl reactions. Each PCR reaction contained ~20ng template DNA, 50pmol each primer and 2.5 units *Pwo* polymerase. Each PCR reaction was carried out in a standard buffer (10mM Tris.HCl pH8.8, 25mM KCl, 5mM $(NH_4)_2SO_4$, 2mM $MgSO_4$, 10% DMSO). Each of the four PCR reactions then

also contained a non-standard deoxynucleotide triphosphate mix, as follows:

At page 18, the paragraph starting at line 20 and ending on page 19, line 4, was replaced with the following:

5'-TAA GGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 5)
5'-TAA AGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 6)
5'-TAA TGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 7)
5'-TAA CGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 8)

5'-TAG GGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 9)
5'-TAG AGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 10)
5'-TAG TGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 11)
5'-TAG CGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 12)

5'-TGA GGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 13)
5'-TGA AGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 14)
5'-TGA TGA AGA GCT AGT ACT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 15)
5'-TGA CGA AGA GCT AGT ACT CCA GAC
Sap I *Bpm* I
TGG CCG TCG TTT TAC-3' (SEQ ID NO: 16)
LMB2 binding site

At page 19, the paragraph starting at line 13 and ending at line 16 was replaced with the following:

5'-TAA NNN NNN ACT CCT CCT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 17)
5'-TAG NNN NNN ACT CCT CCT CCA GAC TGG CCG TCG TTT TAC-3' (SEQ ID NO: 18)

5'-TGA NNN NNN ACT CCT CCT CCA GAC
Bse RI *Bpm* I

TGG CCG TCG TTT TAC-3' (SEQ ID NO: 19)
LMB2 binding site

At page 29, the paragraph starting at line 10 and ending at line 12 was replaced with the following:

κB motif 5'-CGT ATG TTG TGG GGA ATT CCC AGC GGA TAA C-3' (SEQ ID NO: 20)
5'-GTT ATC CGC TGG GAA TTC CCC
NF-κB P50 binding site
ACA ACA TAC G-3' (SEQ ID NO: 21)

At page 31, the paragraph starting at line 22 and ending at line 24 was replaced with the following:

5'-GTA AAA CGA CGG CCA GTC TGG AGG AGG AGA NNN NNN TCA-3' (SEQ ID NO: 22)
5'-GTA AAA CGA CGG CCA GTC TGG AGG AGG AGA NNN NNN TTA-3' (SEQ ID NO: 23)
5'-GTA AAA CGA CGG CCA GTC TGG AGG AGG AGA NNN NNN CTA-3' (SEQ ID NO: 24)

At page 33, the paragraph starting at line 25 and ending at line 25 was replaced with the following:

5'-GTA AAA CGA CGG CCA GTC TGG AGG AGG AGA NNN NNN TCA-3' (SEQ ID NO: 25)

At page 35, the paragraph starting at line 14 and ending at line 16 was replaced with the following:

5'-ATG CTG ACG TCA TGA GGC CCA TGG
Aat II *Bsp* HI *Sfi* I
GGC CCG GAT AAC AAT TTC ACA CAG G-3' (SEQ ID NO: 3)

The existing Sequence Listing has been canceled and replaced with the substitute Sequence Listing attached herewith and which was added at the end of the application.